

H04714.txt
SEQUENZPROTOKOLL

<110> Henkel Kommanditgesellschaft auf Aktien

<120> Wasch- und Reinigungsmittel mit Hybrid-Alpha-Amylasen

<130> H 4714 PCT

<140>

<141>

<150> DE 10138753.9-41

<151> 2001-08-07

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 1452

<212> DNA

<213> Bacillus licheniformis

<220>

<221> CDS

<222> (1)..(1452)

```

<400> 1
gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc 48
Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
1 5 10 15

aat gac ggc caa cat tgg aag cgc ttg caa aac gac tcg gca tat ttg 96
Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu
20 25 30

gct gaa cac ggt att act gcc gtc tgg att ccc ccg gca tat aag gga 144
Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

acg agc caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta 192
Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

ggg gag ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa 240
Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

gga gag ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac 288
Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
85 90 95

gtt tac ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc 336
Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
100 105 110

gaa gat gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta 384
Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
115 120 125

att tca gga gaa cac cga att aaa gcc tgg aca cat ttt cat ttt ccg 432
Ile Ser Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro
130 135 140

```

H04714.txt

ggg cgc ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt 480
 Gly Arg Gly Ser Thr Tyr 150 Ser Asp Phe Lys Trp His Trp Tyr His Phe 160
 145

gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag 528
 Asp Gly Thr Asp Trp 165 Asp Glu Ser Arg Lys 170 Leu Asn Arg Ile Tyr Lys 175

ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac 576
 Phe Gln Gly Lys 180 Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn 190

tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc 624
 Tyr Asp Tyr 195 Leu Met Tyr Ala Asp 200 Ile Asp Tyr Asp His 205 Pro Asp Val

gca gca gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa 672
 Ala Ala Glu Ile Lys Arg Trp 215 Gly Thr Trp Tyr Ala Asn Glu Leu Gln 220

ttg gac ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt 720
 Leu Asp Gly Phe Arg 230 Leu Asp Ala Val Lys His 235 Ile Lys Phe Ser Phe 240

ttg cgg gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg 768
 Leu Arg Asp Trp 245 Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met 255

ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac 816
 Phe Thr Val 260 Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn 270

tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt 864
 Tyr Leu Asn 275 Lys Thr Asn Phe Asn His Ser Val Phe Asp 285 Val Pro Leu

cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg 912
 His Tyr 290 Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met

agg aaa ttg ctg aac agt acg gtc gtt tcc aag cat ccg ttg aaa gcg 960
 Arg Lys Leu Leu Asn Ser 310 Thr Val Val Ser Lys 315 His Pro Leu Lys Ala 320

gtt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag 1008
 Val Thr Phe Val 325 Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu 335

tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc 1056
 Ser Thr Val 340 Gln Thr Trp Phe Lys Pro 345 Leu Ala Tyr Ala Phe Ile Leu 350

aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg 1104
 Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly 365

acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att 1152
 Thr Lys 370 Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile 380

gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat 1200
 Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His

385 390 395 400

gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac 1248
 Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
 405 410 415

agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc 1296
 Ser Ser Val Ala Asn Ser Gly Leu Ala Leu Ile Thr Asp Gly Pro
 420 425 430

ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca 1344
 Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
 435 440 445

tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg 1392
 Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
 450 455 460

gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat 1440
 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480

gtt caa aga tag 1452
 Val Gln Arg

<210> 2

<211> 483

<212> PRT

<213> Bacillus licheniformis

<400> 2

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
 1 5 10 15
 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu
 20 25 30
 Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45
 Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
 50 55 60
 Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 75 80
 Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
 85 90 95
 Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
 100 105 110
 Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
 115 120 125
 Ile Ser Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro
 130 135 140
 Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
 145 150 155 160
 Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
 165 170 175
 Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
 180 185 190
 Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
 195 200 205
 Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
 210 215 220
 Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
 225 230 235 240
 Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met

H04714.txt

Phe Thr Val Ala²⁴⁵ Glu Tyr Trp Gln Asn²⁵⁰ Asp Leu Gly Ala²⁵⁵ Leu Glu Asn
 Tyr Leu Asn²⁶⁰ Lys Thr Asn Phe Asn²⁶⁵ His Ser Val Phe Asp²⁷⁰ Val Pro Leu
 His Tyr Gln²⁷⁵ Phe His Ala Ala²⁸⁰ Ser Thr Gln Gly Gly²⁸⁵ Tyr Asp Met
 Arg²⁹⁰ Lys Leu Leu Asn²⁹⁵ Ser Thr Val Val Ser Lys³⁰⁰ His Pro Leu Lys Ala
 Val³⁰⁵ Thr Phe Val Asp³¹⁰ Asn His Asp Thr Gln³¹⁵ Pro Gly Gln Ser Leu Glu
 Ser Thr Val Gln³²⁵ Thr Trp Phe Lys Pro³³⁰ Leu Ala Tyr Ala³³⁵ Phe Ile Leu
 Thr Arg Glu³⁴⁰ Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp³⁴⁵ Met Tyr Gly
 Thr Lys Gly³⁵⁵ Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys³⁶⁰ His Lys Ile
 Glu³⁷⁰ Pro Ile Leu Lys Ala³⁷⁵ Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
 Asp³⁸⁵ Tyr Phe Asp His³⁹⁰ His Asp Ile Val Gly³⁹⁵ Trp Thr Arg Glu Gly Asp
 Ser Ser Val Ala⁴⁰⁵ Asn Ser Gly Leu Ala⁴¹⁰ Leu Ile Thr Asp Gly Pro
 Gly Gly Ala⁴²⁰ Lys Arg Met Tyr Val Gly Arg Gln Asn Ala⁴²⁵ Gly Glu Thr
 Trp His Asp⁴³⁵ Ile Thr Gly Asn⁴⁴⁰ Arg Ser Glu Pro Val⁴⁴⁵ Ile Asn Ser
 Glu⁴⁵⁰ Gly Trp Gly Glu Phe⁴⁵⁵ His Val Asn Gly Gly⁴⁶⁰ Ser Val Ser Ile Tyr
 Val⁴⁶⁵ Gln Arg⁴⁷⁰

<210> 3

<211> 1452

<212> DNA

<213> Bacillus amyloliquefaciens

<220>

<221> CDS

<222> (1)..(1452)

<400> 3

gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac gac 48
 Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
 1 5 10 15

ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat 96
 Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
 20 25 30

atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc 144
 Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
 35 40 45

caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa 192
 Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
 50 55 60

ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca gag 240
 Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
 65 70 75 80

ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac	288
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr	
85 90 95	
gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat	336
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp	
100 105 110	
gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg	384
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser	
115 120 125	
gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt	432
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg	
130 135 140	
gga aac acg tac agt gat ttt aaa tgg cat tgg tat cat ttc gac gga	480
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly	
145 150 155 160	
gcg gac tgg gat gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt	528
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg	
165 170 175	
ggg gaa gga aaa gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac	576
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn	
180 185 190	
tat gac tat tta atg tat gct gat gtt gac tac gac cac cct gat gtc	624
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val	
195 200 205	
gtg gca gag aca aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca	672
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser	
210 215 220	
tta gac ggc ttc cgt att gat gcc gcc aaa cat att aaa ttt tca ttt	720
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe	
225 230 235 240	
ctg cgt gat tgg gtt cag gcg gtc aga cag gcg acg gga aaa gaa atg	768
Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met	
245 250 255	
ttt acg gtt gcg gag tat tgg cag aat aat gcc ggg aaa ctc gaa aac	816
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn	
260 265 270	
tac ttg aat aaa aca agc ttt aat caa tcc gtg ttt gat gtt ccg ctt	864
Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu	
275 280 285	
cat ttc aat tta cag gcg gct tcc tca caa gga ggc gga tat gat atg	912
His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met	
290 295 300	
agg cgt ttg ctg gac ggt acc gtt gtg tcc agg cat ccg gaa aag gcg	960
Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala	
305 310 315 320	
gtt aca ttt gtt gaa aat cat gac aca cag ccg gga cag tca ttg gaa	1008
Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu	
325 330 335	

H04714.txt

ctt	caa	gat	gcg	atc	ggc	tca	ctg	cat	tcc	cgg	aac	gtc	caa	gta	tac	288
Leu	Gln	Asp	Ala	Ile	Gly	Ser	Leu	His	Ser	Arg	Asn	Val	Gln	Val	Tyr	
				85					90					95		
gga	gat	gtg	gtt	ttg	aat	cat	aag	gct	ggg	gct	gat	gca	aca	gaa	gat	336
Gly	Asp	Val	Val	Leu	Asn	His	Lys	Ala	Gly	Ala	Asp	Ala	Thr	Glu	Asp	
			100					105					110			
gta	act	gcc	gtc	gaa	gtc	aat	ccg	gcc	aat	aga	aat	cag	gaa	act	tcg	384
Val	Thr	Ala	Val	Glu	Val	Asn	Pro	Ala	Asn	Arg	Asn	Gln	Glu	Thr	Ser	
		115					120					125				
gag	gaa	tat	caa	atc	aaa	gcg	tgg	acg	gat	ttt	cgt	ttt	ccg	ggc	cgt	432
Glu	Glu	Tyr	Gln	Ile	Lys	Ala	Trp	Thr	Asp	Phe	Arg	Phe	Pro	Gly	Arg	
	130					135					140					
gga	aac	acg	tac	agt	gat	ttt	aaa	tgg	cat	tgg	tat	cat	ttc	gac	gga	480
Gly	Asn	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly	
					150					155					160	
gcg	gac	tgg	gat	gaa	tcc	cgg	aag	atc	agc	cgc	atc	ttt	aag	ttt	cgt	528
Ala	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Ile	Ser	Arg	Ile	Phe	Lys	Phe	Arg	
				165					170					175		
ggg	gaa	gga	aaa	gcg	tgg	gat	tgg	gaa	gta	tca	agt	gaa	aac	ggc	aac	576
Gly	Glu	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Ser	Glu	Asn	Gly	Asn	
			180					185					190			
tat	gac	tat	tta	atg	tat	gct	gat	gtt	gac	tac	gac	cac	cct	gat	gtc	624
Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Val	Asp	Tyr	Asp	His	Pro	Asp	Val	
		195					200					205				
gtg	gca	gag	aca	aaa	aaa	tgg	ggg	atc	tgg	tat	gcg	aat	gaa	ctg	tca	672
Val	Ala	Glu	Thr	Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	Leu	Ser	
						215					220					
tta	gac	ggc	ttc	cgt	att	gat	gcc	gcc	aaa	cat	att	aaa	ttt	tca	ttt	720
Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	Ser	Phe	
					230					235					240	
ctg	cgt	gat	tgg	gtt	cag	gcg	gtc	aga	cag	gcg	acg	gga	aaa	gaa	atg	768
Leu	Arg	Asp	Trp	Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	Glu	Met	
				245					250					255		
ttt	acg	gtt	gcg	gag	tat	tgg	cag	aat	aat	gcc	ggg	aaa	ctc	gaa	aac	816
Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asn	Ala	Gly	Lys	Leu	Glu	Asn	
			260					265					270			
tac	ttg	aat	aaa	aca	agc	ttt	aat	caa	tcc	gtg	ttt	gat	gtt	ccg	ctt	864
Tyr	Leu	Asn	Lys	Thr	Ser	Phe	Asn	Gln	Ser	Val	Phe	Asp	Val	Pro	Leu	
		275					280					285				
cat	ttc	aat	tta	cag	gcg	gct	tcc	tca	caa	gga	ggc	gga	tat	gat	atg	912
His	Phe	Asn	Leu	Gln	Ala	Ala	Ser	Ser	Gln	Gly	Gly	Gly	Tyr	Asp	Met	
					295						300					
agg	cgt	ttg	ctg	gac	ggg	acc	gtt	gtg	tcc	agg	cat	ccg	gaa	aag	gcg	960
Arg	Arg	Leu	Leu	Asp	Gly	Thr	Val	Val	Ser	Arg	His	Pro	Glu	Lys	Ala	
	305				310					315					320	
gtt	aca	ttt	gtt	gaa	aat	cat	gac	aca	cag	ccg	gga	cag	tca	ttg	gaa	1008
Val	Thr	Phe	Val	Glu	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	
				325					330					335		

H04714.txt

tcg	aca	gtc	caa	act	tgg	ttt	aaa	ccg	ctt	gca	tac	gcc	ttt	att	ttg	1056
Ser	Thr	Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	
		340						345					350			
aca	aga	gaa	tcc	ggt	tat	cct	cag	gtg	ttc	tat	ggg	gat	atg	tac	ggg	1104
Thr	Arg	Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	
		355					360					365				
aca	aaa	ggg	aca	tcg	cca	aag	gaa	att	ccc	tca	ctg	aaa	gat	aat	ata	1152
Thr	Lys	Gly	Thr	Ser	Pro	Lys	Glu	Ile	Pro	Ser	Leu	Lys	Asp	Asn	Ile	
	370					375					380					
gag	ccg	att	tta	aaa	gcg	cgt	aag	gag	tac	gca	tac	ggg	ccc	cag	cac	1200
Glu	Pro	Ile	Leu	Lys	Ala	Arg	Lys	Glu	Tyr	Ala	Tyr	Gly	Pro	Gln	His	
385					390					395					400	
gat	tat	att	gac	cac	ccg	gat	gtg	atc	gga	tgg	acg	agg	gaa	ggt	gac	1248
Asp	Tyr	Ile	Asp	His	Pro	Asp	Val	Ile	Gly	Trp	Thr	Arg	Glu	Gly	Asp	
				405					410					415		
agc	tcc	gcc	gcc	aaa	tca	ggt	ttg	gcc	gct	tta	atc	acg	gac	gga	ccc	1296
Ser	Ser	Ala	Ala	Lys	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro	
			420					425					430			
ggc	gga	tca	aag	cgg	atg	tat	gcc	ggc	ctg	aaa	aat	gcc	ggc	gag	aca	1344
Gly	Gly	Ser	Lys	Arg	Met	Tyr	Ala	Gly	Leu	Lys	Asn	Ala	Gly	Glu	Thr	
		435					440					445				
tgg	tat	gac	ata	acg	ggc	aac	cgt	tca	gat	act	gta	aaa	atc	gga	tct	1392
Trp	Tyr	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Asp	Thr	Val	Lys	Ile	Gly	Ser	
	450					455					460					
gac	ggc	tgg	gga	gag	ttt	cat	gta	aac	gat	ggg	tcc	gtc	tcc	att	tat	1440
Asp	Gly	Trp	Gly	Glu	Phe	His	Val	Asn	Asp	Gly	Ser	Val	Ser	Ile	Tyr	
465					470					475					480	
ggt	cag	aaa	taa													1452
Val	Gln	Lys														

<210> 4

<211> 483

<212> PRT

<213> Bacillus amyloliquefaciens

<400> 4

Val	Asn	Gly	Thr	Leu	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	Thr	Pro	Asn	Asp	
1				5					10					15		
Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu	Ser	Asp	
			20					25					30			
Ile	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	Leu	Ser	
		35				40						45				
Gln	Ser	Asp	Asn	Gly	Tyr	Gly	Pro	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu	
	50					55					60					
Phe	Gln	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Ser	Glu	
65					70				75						80	
Leu	Gln	Asp	Ala	Ile	Gly	Ser	Leu	His	Ser	Arg	Asn	Val	Gln	Val	Tyr	
				85					90					95		
Gly	Asp	Val	Val	Leu	Asn	His	Lys	Ala	Gly	Ala	Asp	Ala	Thr	Glu	Asp	
		100					105						110			
Val	Thr	Ala	Val	Glu	Val	Asn	Pro	Ala	Asn	Arg	Asn	Gln	Glu	Thr	Ser	
		115					120					125				

H04714.txt

Glu	Glu	Tyr	Gln	Ile	Lys	Ala	Trp	Thr	Asp	Phe	Arg	Phe	Pro	Gly	Arg
	130					135					140				
Gly	Asn	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly
145					150					155					160
Ala	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Ile	Ser	Arg	Ile	Phe	Lys	Phe	Arg
				165						170					175
Gly	Glu	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Ser	Glu	Asn	Gly	Asn
			180					185					190		
Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Val	Asp	Tyr	Asp	His	Pro	Asp	Val
		195					200					205			
Val	Ala	Glu	Thr	Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	Leu	Ser
	210					215					220				
Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	Ser	Phe
225					230					235					240
Leu	Arg	Asp	Trp	Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	Glu	Met
				245					250					255	
Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Ala	Gly	Lys	Leu	Glu	Asn	
			260					265					270		
Tyr	Leu	Asn	Lys	Thr	Ser	Phe	Asn	Gln	Ser	Val	Phe	Asp	Val	Pro	Leu
		275					280					285			
His	Phe	Asn	Leu	Gln	Ala	Ala	Ser	Ser	Gln	Gly	Gly	Gly	Tyr	Asp	Met
	290				295						300				
Arg	Arg	Leu	Leu	Asp	Gly	Thr	Val	Val	Ser	Arg	His	Pro	Glu	Lys	Ala
305					310					315					320
Val	Thr	Phe	Val	Glu	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu
				325					330					335	
Ser	Thr	Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu
			340					345					350		
Thr	Arg	Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly
		355					360					365			
Thr	Lys	Gly	Thr	Ser	Pro	Lys	Glu	Ile	Pro	Ser	Leu	Lys	Asp	Asn	Ile
	370					375					380				
Glu	Pro	Ile	Leu	Lys	Ala	Arg	Lys	Glu	Tyr	Ala	Tyr	Gly	Pro	Gln	His
385					390					395					400
Asp	Tyr	Ile	Asp	His	Pro	Asp	Val	Ile	Gly	Trp	Thr	Arg	Glu	Gly	Asp
				405					410					415	
Ser	Ser	Ala	Ala	Lys	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro
			420					425					430		
Gly	Gly	Ser	Lys	Arg	Met	Tyr	Ala	Gly	Leu	Lys	Asn	Ala	Gly	Glu	Thr
		435					440					445			
Trp	Tyr	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Asp	Thr	Val	Lys	Ile	Gly	Ser
	450					455					460				
Asp	Gly	Trp	Gly	Glu	Phe	His	Val	Asn	Asp	Gly	Ser	Val	Ser	Ile	Tyr
465					470					475					480
Val	Gln	Lys													

<210> 5
 <211> 1446
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen Sequenz:Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (AL34).

<220>
 <221> CDS
 <222> (1)..(1446)

<400> 5

H04714.txt

gta	aat	ggc	acg	ctg	atg	cag	tat	ttt	gaa	tgg	tat	acg	ccg	aac	gac	48
Val	Asn	Gly	Thr	Leu	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	Thr	Pro	Asn	Asp	
1				5					10					15		
ggc	cag	cat	tgg	aaa	cga	ttg	cag	aat	gat	gcg	gaa	cat	tta	tcg	gat	96
Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu	Ser	Asp	
			20					25					30			
atc	ggc	att	act	gcc	gtc	tgg	att	ccc	ccg	gca	tat	aag	gga	acg	agc	144
Ile	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	Thr	Ser	
		35					40					45				
caa	gcg	gat	gtg	ggc	tac	ggt	gct	tac	gac	ctt	tat	gat	tta	ggg	gag	192
Gln	Ala	Asp	Val	Gly	Tyr	Gly	Ala	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu	
	50					55					60					
ttt	cat	caa	aaa	ggg	acg	gtt	cgg	aca	aag	tac	ggc	aca	aaa	gga	gag	240
Phe	His	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Gly	Glu	
65					70					75					80	
ctg	caa	tct	gcg	atc	aaa	agt	ctt	cat	tcc	cgc	gac	att	aac	gtt	tac	288
Leu	Gln	Ser	Ala	Ile	Lys	Ser	Leu	His	Ser	Arg	Asp	Ile	Asn	Val	Tyr	
				85					90					95		
ggg	gat	gtg	gtc	atc	aac	cac	aaa	ggc	ggc	gct	gat	gcg	acc	gaa	gat	336
Gly	Asp	Val	Val	Ile	Asn	His	Lys	Gly	Gly	Ala	Asp	Ala	Thr	Glu	Asp	
			100					105					110			
gta	acc	gcg	gtt	gaa	gtc	gat	ccc	gct	gac	cgc	aac	cgc	gta	att	tca	384
Val	Thr	Ala	Val	Glu	Val	Asp	Pro	Ala	Asp	Arg	Asn	Arg	Val	Ile	Ser	
		115					120					125				
gga	gaa	cac	cga	att	aaa	gcc	tgg	aca	cat	ttt	cat	ttt	ccg	ggg	cgc	432
Gly	Glu	His	Arg	Ile	Lys	Ala	Trp	Thr	His	Phe	His	Phe	Pro	Gly	Arg	
	130					135					140					
ggc	agc	aca	tac	agc	gat	ttt	aaa	tgg	cat	tgg	tac	cat	ttt	gac	gga	480
Gly	Ser	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly	
145					150					155					160	
acc	gat	tgg	gac	gag	tcc	cga	aag	ctg	aac	cgc	atc	tat	aag	ttt	caa	528
Thr	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Asn	Arg	Ile	Tyr	Lys	Phe	Gln	
				165					170					175		
gga	aag	gct	tgg	gat	tgg	gaa	gtt	tcc	aat	gaa	aac	ggc	aac	tat	gat	576
Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Asn	Glu	Asn	Gly	Asn	Tyr	Asp	
			180					185					190			
tat	ttg	atg	tat	gcc	gac	atc	gat	tat	gac	cat	cct	gat	gtc	gca	gca	624
Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Tyr	Asp	His	Pro	Asp	Val	Ala	Ala	
		195					200					205				
gaa	att	aag	aga	tgg	ggc	act	tgg	tat	gcc	aat	gaa	ctg	caa	ttg	gac	672
Glu	Ile	Lys	Arg	Trp	Gly	Thr	Trp	Tyr	Ala	Asn	Glu	Leu	Gln	Leu	Asp	
	210					215					220					
ggt	ttc	cgt	ctt	gat	gct	gtc	aaa	cac	att	aaa	ttt	tct	ttt	ttg	cgg	720
Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe	Leu	Arg	
225					230					235					240	
gat	tgg	gtt	aat	cat	gtc	agg	gaa	aaa	acg	ggg	aag	gaa	atg	ttt	acg	768
Asp	Trp	Val	Asn	His	Val	Arg	Glu	Lys	Thr	Gly	Lys	Glu	Met	Phe	Thr	
				245					250					255		

H04714.txt

gta	gct	gaa	tat	tgg	cag	aat	gac	ttg	ggc	gcg	ctg	gaa	aac	tat	ttg	816
Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn	Tyr	Leu	
			260					265					270			
aac	aaa	aca	aat	ttt	aat	cat	tca	gtg	ttt	gac	gtg	ccg	ctt	cat	tat	864
Asn	Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Tyr	
		275					280					285				
cag	ttc	cat	gct	gca	tcg	aca	cag	gga	ggc	ggc	tat	gat	atg	agg	aaa	912
Gln	Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met	Arg	Lys	
	290					295					300					
ttg	ctg	aac	agt	acg	gtc	gtt	tcc	aag	cat	ccg	ttg	aaa	gcg	gtt	aca	960
Leu	Leu	Asn	Ser	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ala	Val	Thr	
305					310					315					320	
ttt	gtc	gat	aac	cat	gat	aca	cag	ccg	ggg	caa	tcg	ctt	gag	tcg	act	1008
Phe	Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	Ser	Thr	
				325					330					335		
gtc	caa	aca	tgg	ttt	aag	ccg	ctt	gct	tac	gct	ttt	att	ctc	aca	agg	1056
Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Arg	
			340					345					350			
gaa	tct	gga	tac	cct	cag	gtt	ttc	tac	ggg	gat	atg	tac	ggg	acg	aaa	1104
Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	Thr	Lys	
		355					360					365				
gga	gac	tcc	cag	cgc	gaa	att	cct	gcc	ttg	aaa	cac	aaa	att	gaa	ccg	1152
Gly	Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile	Glu	Pro	
		370				375					380					
atc	tta	aaa	gcg	aga	aaa	cag	tat	gcg	tac	gga	gca	cag	cat	gat	tat	1200
Ile	Leu	Lys	Ala	Arg	Lys	Gln	Tyr	Ala	Tyr	Gly	Ala	Gln	His	Asp	Tyr	
385					390					395					400	
ttc	gac	cac	cat	gac	att	gtc	ggc	tgg	aca	agg	gaa	ggc	gac	agc	tcg	1248
Phe	Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp	Ser	Ser	
				405				410						415		
gtt	gca	aat	tca	ggt	ttg	gcg	gca	tta	ata	aca	gac	gga	ccc	ggt	ggg	1296
Val	Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro	Gly	Gly	
			420					425					430			
gca	aag	cga	atg	tat	gtc	ggc	cgg	caa	aac	gcc	ggt	gag	aca	tgg	cat	1344
Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr	Trp	His	
		435					440					445				
gac	att	acc	gga	aac	cgt	tcg	gag	ccg	gtt	gtc	atc	aat	tcg	gaa	ggc	1392
Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser	Glu	Gly	
	450					455					460					
tgg	gga	gag	ttt	cac	gta	aac	ggc	ggg	tcg	gtt	tca	att	tat	gtt	caa	1440
Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr	Val	Gln	
465					470					475					480	
aga	tag															1446
Arg																

<210> 6
<211> 481

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz:Fusion der
Alpha-Amylase-Gene von B. licheniformis und B.
amyloliquefaciens (AL34).

<400> 6

```

Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
 1      5      10      15
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
 20      25      30
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser
 35      40      45
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu
 50      55      60
Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu
 65      70      75      80
Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr
 85      90      95
Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp
100      105      110
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser
115      120      125
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg
130      135      140
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145      150      155      160
Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln
165      170      175
Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp
180      185      190
Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala
195      200      205
Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp
210      215      220
Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg
225      230      235      240
Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr
245      250      255
Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu
260      265      270
Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr
275      280      285
Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
290      295      300
Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala Val Thr
305      310      315
Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr
320      325      330
Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg
335      340      345
Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
350      355      360
Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
365      370      375
Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr
380      385      390      395
Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
400      405      410
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly
415      420      425
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His
430      435      440      445

```

H04714.txt

Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser	Glu	Gly
	450					455					460				
Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr	Val	Gln
465					470					475					480
Arg															

<210> 7
 <211> 1446
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen Sequenz:Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (AL76).

<220>
 <221> CDS
 <222> (1)..(1446)

<400> 7																	
gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac gac	48																
Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp																	
1 5 10 15																	
ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat	96																
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp																	
20 25 30																	
atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc	144																
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser																	
35 40 45																	
caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa	192																
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu																	
50 55 60																	
ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa gga gag	240																
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu																	
65 70 75 80																	
ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac gtt tac	288																
Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr																	
85 90 95																	
ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc gaa gat	336																
Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp																	
100 105 110																	
gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta att tca	384																
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser																	
115 120 125																	
gga gaa cac cga att aaa gcc tgg aca cat ttt cat ttt ccg ggg cgc	432																
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg																	
130 135 140																	
ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt gac gga	480																
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly																	
145 150 155 160																	

H04714.txt

acc	gat	tgg	gac	gag	tcc	cga	aag	ctg	aac	cgc	atc	tat	aag	ttt	caa	528
Thr	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Asn	Arg	Ile	Tyr	Lys	Phe	Gln	
				165					170					175		
gga	aag	gct	tgg	gat	tgg	gaa	gtt	tcc	aat	gaa	aac	ggc	aac	tat	gat	576
Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Asn	Glu	Asn	Gly	Asn	Tyr	Asp	
			180					185					190			
tat	ttg	atg	tat	gcc	gac	atc	gat	tat	gac	cat	cct	gat	gtc	gca	gca	624
Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Tyr	Asp	His	Pro	Asp	Val	Ala	Ala	
		195					200					205				
gaa	att	aag	aga	tgg	ggc	act	tgg	tat	gcc	aat	gaa	ctg	caa	ttg	gac	672
Glu	Ile	Lys	Arg	Trp	Gly	Thr	Trp	Tyr	Ala	Asn	Glu	Leu	Gln	Leu	Asp	
	210					215					220					
ggt	ttc	cgt	ctt	gat	gct	gtc	aaa	cac	att	aaa	ttt	tct	ttt	ttg	cgg	720
Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe	Leu	Arg	
					230					235					240	
gat	tgg	gtt	aat	cat	gtc	agg	gaa	aaa	acg	ggg	aag	gaa	atg	ttt	acg	768
Asp	Trp	Val	Asn	His	Val	Arg	Glu	Lys	Thr	Gly	Lys	Glu	Met	Phe	Thr	
				245					250					255		
gta	gct	gaa	tat	tgg	cag	aat	gac	ttg	ggc	gcg	ctg	gaa	aac	tat	ttg	816
Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn	Tyr	Leu	
			260					265					270			
aac	aaa	aca	aat	ttt	aat	cat	tca	gtg	ttt	gac	gtg	ccg	ctt	cat	tat	864
Asn	Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Tyr	
		275					280					285				
cag	ttc	cat	gct	gca	tcg	aca	cag	gga	ggc	ggc	tat	gat	atg	agg	aaa	912
Gln	Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met	Arg	Lys	
	290					295					300					
ttg	ctg	aac	agt	acg	gtc	gtt	tcc	aag	cat	ccg	ttg	aaa	gcg	gtt	aca	960
Leu	Leu	Asn	Ser	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ala	Val	Thr	
	305				310					315					320	
ttt	gtc	gat	aac	cat	gat	aca	cag	ccg	ggg	caa	tcg	ctt	gag	tcg	act	1008
Phe	Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	Ser	Thr	
				325					330					335		
gtc	caa	aca	tgg	ttt	aag	ccg	ctt	gct	tac	gct	ttt	att	ctc	aca	agg	1056
Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Arg	
			340					345					350			
gaa	tct	gga	tac	cct	cag	gtt	ttc	tac	ggg	gat	atg	tac	ggg	acg	aaa	1104
Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	Thr	Lys	
		355				360						365				
gga	gac	tcc	cag	cgc	gaa	att	cct	gcc	ttg	aaa	cac	aaa	att	gaa	ccg	1152
Gly	Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile	Glu	Pro	
						375					380					
atc	tta	aaa	gcg	aga	aaa	cag	tat	gcg	tac	gga	gca	cag	cat	gat	tat	1200
Ile	Leu	Lys	Ala	Arg	Lys	Gln	Tyr	Ala	Tyr	Gly	Ala	Gln	His	Asp	Tyr	
					390					395				400		
ttc	gac	cac	cat	gac	att	gtc	ggc	tgg	aca	agg	gaa	ggc	gac	agc	tcg	1248
Phe	Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp	Ser	Ser	
				405					410					415		

H04714.txt

gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc ggt ggg	1296
Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly	
	420 425 430
gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca tgg cat	1344
Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His	
	435 440 445
gac att acc gga aac cgt tgc gag ccg gtt gtc atc aat tcg gaa ggc	1392
Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly	
	450 455 460
tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat gtt caa	1440
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln	
	465 470 475 480
aga tag	1446
Arg	

<210> 8
 <211> 481
 <212> PRT
 <213> Künstliche Sequenz
 <223> Beschreibung der künstlichen Sequenz:Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (AL76).

<400> 8

Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp	
1 5 10 15	
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp	
20 25 30	
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser	
35 40 45	
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu	
50 55 60	
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu	
65 70 75 80	
Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr	
85 90 95	
Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp	
100 105 110	
Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser	
115 120 125	
Gly Glu His Arg Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg	
130 135 140	
Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly	
145 150 155 160	
Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln	
165 170 175	
Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp	
180 185 190	
Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala	
195 200 205	
Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp	
210 215 220	
Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg	
225 230 235 240	
Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr	
245 250 255	
Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu	

H04714.txt

Asn	Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Tyr
		275					280					285			
Gln	Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met	Arg	Lys
	290					295					300				
Leu	Leu	Asn	Ser	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ala	Val	Thr
305					310					315					320
Phe	Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	Ser	Thr
				325					330					335	
Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Arg
			340					345					350		
Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	Thr	Lys
		355					360					365			
Gly	Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile	Glu	Pro
	370					375					380				
Ile	Leu	Lys	Ala	Arg	Lys	Gln	Tyr	Ala	Tyr	Gly	Ala	Gln	His	Asp	Tyr
385					390					395					400
Phe	Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp	Ser	Ser
				405					410					415	
Val	Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro	Gly	Gly
			420					425					430		
Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr	Trp	His
		435						440				445			
Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser	Glu	Gly
	450					455					460				
Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr	Val	Gln
465					470					475					480
Arg															

<210> 9

<211> 1446

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz: Fusion der Alpha-Amylase-Gene von B. licheniformis und B. amyloliquefaciens (AL112).

<220>

<221> CDS

<222> (1)..(1446)

<400> 9

gta	aat	ggc	acg	ctg	atg	cag	tat	ttt	gaa	tgg	tat	acg	ccg	aac	gac	48
Val	Asn	Gly	Thr	Leu	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	Thr	Pro	Asn	Asp	
1				5					10					15		

ggc	cag	cat	tgg	aaa	cga	ttg	cag	aat	gat	gcg	gaa	cat	tta	tcg	gat	96
Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu	Ser	Asp	
			20					25					30			

atc	gga	atc	act	gcc	gtc	tgg	att	cct	ccc	gca	tac	aaa	gga	ttg	agc	144
Ile	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	Leu	Ser	
			35				40					45				

caa	tcc	gat	aac	gga	tac	gga	cct	tat	gat	ttg	tat	gat	tta	gga	gaa	192
Gln	Ser	Asp	Asn	Gly	Tyr	Gly	Pro	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu	
		50				55					60					

ttc	cag	caa	aaa	ggg	acg	gtc	aga	acg	aaa	tac	ggc	aca	aaa	tca	gag	240
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

H04714.txt

Phe 65	Gln	Gln	Lys	Gly	Thr 70	Val	Arg	Thr	Lys	Tyr 75	Gly	Thr	Lys	Ser	Glu 80	
ctt Leu	caa Gln	gat Asp	gcg Ala	atc Ile 85	ggc Gly	tca Ser	ctg Leu	cat His	tcc Ser 90	cgg Arg	aac Asn	gtc Val	caa Gln	gta Val 95	tac Tyr	288
gga Gly	gat Asp	gtg Val	gtt Val 100	ttg Leu	aat Asn	cat His	aag Lys	gct Ala 105	ggt Gly	gct Ala	gat Asp	gca Ala	aca Thr 110	gaa Glu	gat Asp	336
gta Val	acc Thr	gcg Ala 115	gtt Val	gaa Glu	gtc Val	gat Asp	ccc Pro 120	gct Ala	gac Asp	cgc Arg	aac Asn	cgc Arg 125	gta Val	att Ile	tca Ser	384
gga Gly	gaa Glu 130	cac His	cga Arg	att Ile	aaa Lys	gcc Ala 135	tgg Trp	aca Thr	cat His	ttt Phe	cat His 140	ttt Phe	ccg Pro	ggg Gly	cgc Arg	432
ggc Gly 145	agc Ser	aca Thr	tac Tyr	agc Ser	gat Asp 150	ttt Phe	aaa Lys	tgg Trp	cat His	tgg Trp 155	tac Tyr	cat His	ttt Phe	gac Asp	gga Gly 160	480
acc Thr	gat Asp	tgg Trp	gac Asp	gag Glu 165	tcc Ser	cga Arg	aag Lys	ctg Leu	aac Asn 170	cgc Arg	atc Ile	tat Tyr	aag Lys	ttt Phe 175	caa Gln	528
gga Gly	aag Lys	gct Ala	tgg Trp 180	gat Asp	tgg Trp	gaa Glu	gtt Val	tcc Ser 185	aat Asn	gaa Glu	aac Asn	ggc Gly 190	aac Asn	tat Tyr	gat Asp	576
tat Tyr	ttg Leu	atg Met 195	tat Tyr	gcc Ala	gac Asp	atc Ile	gat Asp 200	tat Tyr	gac Asp	cat His	cct Pro	gat Asp 205	gtc Val	gca Ala	gca Ala	624
gaa Glu	att Ile 210	aag Lys	aga Arg	tgg Trp	ggc Gly	act Thr 215	tgg Trp	tat Tyr	gcc Ala	aat Asn	gaa Glu 220	ctg Leu	caa Gln	ttg Leu	gac Asp	672
ggt Gly 225	ttc Phe	cgt Arg	ctt Leu	gat Asp	gct Ala 230	gtc Val	aaa Lys	cac His	att Ile	aaa Lys 235	ttt Phe	tct Ser	ttt Phe	ttg Leu	cgg Arg 240	720
gat Asp	tgg Trp	gtt Val	aat Asn	cat His 245	gtc Val	agg Arg	gaa Glu	aaa Lys	acg Thr 250	ggg Gly	aag Lys	gaa Glu	atg Met	ttt Phe 255	acg Thr	768
gta Val	gct Ala	gaa Glu	tat Tyr 260	tgg Trp	cag Gln	aat Asn	gac Asp	ttg Leu 265	ggc Gly	gcg Ala	ctg Leu	gaa Glu	aac Asn 270	tat Tyr	ttg Leu	816
aac Asn	aaa Lys	aca Thr 275	aat Asn	ttt Phe	aat Asn	cat His	tca Ser 280	gtg Val	ttt Phe	gac Asp	gtg Val	ccg Pro 285	ctt Leu	cat His	tat Tyr	864
cag Gln	ttc Phe 290	cat His	gct Ala	gca Ala	tcg Ser	aca Thr 295	cag Gln	gga Gly	ggc Gly	ggc Gly	tat Tyr 300	gat Asp	atg Met	agg Arg	aaa Lys	912
ttg Leu 305	ctg Leu	aac Asn	agt Ser	acg Thr	gtc Val 310	gtt Val	tcc Ser	aag Lys	cat His	ccg Pro 315	ttg Leu	aaa Lys	gcg Ala	gtt Val	aca Thr 320	960

H04714.txt

ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag tcg act	1008
Phe Val Asp Asn His 325 Asp Thr Gln Pro Gly 330 Gln Ser Leu Glu Ser 335 Thr	
gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc aca agg	1056
Val Gln Thr Trp 340 Phe Lys Pro Leu Ala 345 Tyr Ala Phe Ile Leu 350 Thr Arg	
gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg acg aaa	1104
Glu Ser Gly 355 Tyr Pro Gln Val Phe 360 Tyr Gly Asp Met Tyr 365 Gly Thr Lys	
gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att gaa ccg	1152
Gly Asp 370 Ser Gln Arg Glu 375 Ile Pro Ala Leu Lys 380 His Lys Ile Glu Pro	
atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat gat tat	1200
Ile Leu Lys Ala Arg 390 Gln Tyr Ala Tyr 395 Gly Ala Gln His Asp Tyr 400	
ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac agc tcg	1248
Phe Asp His His 405 Ile Val Gly Trp 410 Thr Arg Glu Gly Asp 415 Ser Ser	
gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc ggt ggg	1296
Val Ala Asn Ser 420 Gly Leu Ala Ala Leu 425 Ile Thr Asp Gly Pro 430 Gly Gly	
gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca tgg cat	1344
Ala Lys Arg Met Tyr Val Gly Arg 440 Gln Asn Ala Gly 445 Glu Thr Trp His	
gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg gaa ggc	1392
Asp Ile Thr Gly Asn Arg 455 Ser Glu Pro Val Val 460 Ile Asn Ser Glu Gly	
tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat gtt caa	1440
Trp Gly Glu Phe His 470 Val Asn Gly Gly Ser 475 Val Ser Ile Tyr Val 480 Gln	
aga tag	1446
Arg	

<210> 10
 <211> 481
 <212> PRT
 <213> Künstliche Sequenz
 <223> Beschreibung der künstlichen Sequenz: Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (AL112).

<400> 10
 Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
 1 5 10 15
 Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
 20 25 30
 Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
 35 40 45
 Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
 50 55 60
 Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
 65 70 75 80

H04714.txt

Leu	Gln	Asp	Ala	Ile	Gly	Ser	Leu	His	Ser	Arg	Asn	Val	Gln	Val	Tyr
				85					90					95	
Gly	Asp	Val	Val	Leu	Asn	His	Lys	Ala	Gly	Ala	Asp	Ala	Thr	Glu	Asp
			100					105					110		
Val	Thr	Ala	Val	Glu	Val	Asp	Pro	Ala	Asp	Arg	Asn	Arg	Val	Ile	Ser
		115					120					125			
Gly	Glu	His	Arg	Ile	Lys	Ala	Trp	Thr	His	Phe	His	Phe	Pro	Gly	Arg
	130					135					140				
Gly	Ser	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly
145					150					155					160
Thr	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Asn	Arg	Ile	Tyr	Lys	Phe	Gln
				165					170					175	
Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Asn	Glu	Asn	Gly	Asn	Tyr	Asp
			180					185					190		
Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Tyr	Asp	His	Pro	Asp	Val	Ala	Ala
		195					200					205			
Glu	Ile	Lys	Arg	Trp	Gly	Thr	Trp	Tyr	Ala	Asn	Glu	Leu	Gln	Leu	Asp
	210					215					220				
Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe	Leu	Arg
225					230					235					240
Asp	Trp	Val	Asn	His	Val	Arg	Glu	Lys	Thr	Gly	Lys	Glu	Met	Phe	Thr
				245					250					255	
Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn	Tyr	Leu
			260					265					270		
Asn	Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Tyr
		275					280					285			
Gln	Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met	Arg	Lys
	290					295					300				
Leu	Leu	Asn	Ser	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ala	Val	Thr
305					310					315					320
Phe	Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	Ser	Thr
				325					330					335	
Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Arg
			340					345					350		
Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	Thr	Lys
		355					360					365			
Gly	Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile	Glu	Pro
	370					375					380				
Ile	Leu	Lys	Ala	Arg	Lys	Gln	Tyr	Ala	Tyr	Gly	Ala	Gln	His	Asp	Tyr
385					390					395					400
Phe	Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp	Ser	Ser
				405					410					415	
Val	Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro	Gly	Gly
			420					425					430		
Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr	Trp	His
		435					440					445			
Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser	Glu	Gly
	450					455					460				
Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr	Val	Gln
465					470					475					480
Arg															

<210> 11
 <211> 1452
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen Sequenz: Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (AL256).

<220>

<221> CDS

<222> (1)..(1452)

<400> 11

gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac gac	48
Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp	
1 5 10 15	
ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat	96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp	
20 25 30	
atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga ttg agc	144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser	
35 40 45	
caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga gaa	192
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu	
50 55 60	
ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca gag	240
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu	
65 70 75 80	
ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac	288
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr	
85 90 95	
gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat	336
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp	
100 105 110	
gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg	384
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser	
115 120 125	
gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt	432
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg	
130 135 140	
gga aac acg tac agt gat ttt aaa tgg cat tgg tat cat ttc gac gga	480
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly	
145 150 155 160	
gcg gac tgg gat gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt	528
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg	
165 170 175	
ggg gaa gga aaa gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac	576
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn	
180 185 190	
tat gac tat tta atg tat gct gat gtt gac tac gac cac cct gat gtc	624
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val	
195 200 205	
gtg gca gag aca aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca	672
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser	
210 215 220	
tta gac ggc ttc cgt att gat gcc gcc aaa cat att aaa ttt tca ttt	720

H04714.txt

Leu 225	Asp	Gly	Phe	Arg	Ile 230	Asp	Ala	Ala	Lys	His 235	Ile	Lys	Phe	Ser	Phe 240	
ctg Leu	cgt Arg	gat Asp	tgg Trp	gtt Val 245	cag Gln	gcg Ala	gtc Val	aga Arg	cag Gln 250	gcg Ala	acg Thr	gga Gly	aaa Lys	gaa Glu 255	atg Met	768
ttt Phe	acg Thr	gta Val	gct Ala 260	gaa Glu	tat Tyr	tgg Trp	cag Gln	aat Asn 265	gac Asp	ttg Leu	ggc Gly	gcg Ala	ctg Leu 270	gaa Glu	aac Asn	816
tat Tyr	ttg Leu	aac Asn 275	aaa Lys	aca Thr	aat Asn	ttt Phe	aat Asn 280	cat His	tca Ser	gtg Val	ttt Phe	gac Asp 285	gtg Val	ccg Pro	ctt Leu	864
cat His	tat Tyr 290	cag Gln	ttc Phe	cat His	gct Ala	gca Ala 295	tcg Ser	aca Thr	cag Gln	gga Gly	ggc Gly 300	ggc Gly	tat Tyr	gat Asp	atg Met	912
agg Arg 305	aaa Lys	ttg Leu	ctg Leu	aac Asn	agt Ser 310	acg Thr	gtc Val	gtt Val	tcc Ser	aag Lys 315	cat His	ccg Pro	ttg Leu	aaa Lys	gcg Ala 320	960
gtt Val	aca Thr	ttt Phe	gtc Val	gat Asp 325	aac Asn	cat His	gat Asp	aca Thr	cag Gln 330	ccg Pro	ggg Gly	caa Gln	tcg Ser	ctt Leu 335	gag Glu	1008
tcg Ser	act Thr	gtc Val	caa Gln 340	aca Thr	tgg Trp	ttt Phe	aag Lys	ccg Pro 345	ctt Leu	gct Ala	tac Tyr	gct Ala	ttt Phe 350	att Ile	ctc Leu	1056
aca Thr	agg Arg	gaa Glu 355	tct Ser	gga Gly	tac Tyr	cct Pro	cag Gln 360	gtt Val	ttc Phe	tac Tyr	ggg Gly	gat Asp 365	atg Met	tac Tyr	ggg Gly	1104
acg Thr	aaa Lys 370	gga Gly	gac Asp	tcc Ser	cag Gln	cgc Arg 375	gaa Glu	att Ile	cct Pro	gcc Ala	ttg Leu 380	aaa Lys	cac His	aaa Lys	att Ile	1152
gaa Glu 385	ccg Pro	atc Ile	tta Leu	aaa Lys	gcg Ala 390	aga Arg	aaa Lys	cag Gln	tat Tyr	gcg Ala 395	tac Tyr	gga Gly	gca Ala	cag Gln	cat His 400	1200
gat Asp	tat Tyr	ttc Phe	gac Asp	cac His 405	cat His	gac Asp	att Ile	gtc Val	ggc Gly 410	tgg Trp	aca Thr	agg Arg	gaa Glu	ggc Gly 415	gac Asp	1248
agc Ser	tcg Ser	gtt Val	gca Ala 420	aat Asn	tca Ser	ggt Gly	ttg Leu 425	gcg Ala	gca Ala	tta Leu	ata Ile	aca Thr	gac Asp 430	gga Gly	ccc Pro	1296
ggt Gly	ggg Gly	gca Ala 435	aag Lys	cga Arg	atg Met	tat Tyr	gtc Val 440	ggc Gly	cgg Arg	caa Gln	aac Asn	gcc Ala 445	ggt Gly	gag Glu	aca Thr	1344
tgg Trp	cat His 450	gac Asp	att Ile	acc Thr	gga Gly	aac Asn 455	cgt Arg	tcg Ser	gag Glu	ccg Pro	gtt Val 460	gtc Val	atc Ile	aat Asn	tcg Ser	1392
gaa Glu 465	ggc Gly	tgg Trp	gga Gly	gag Glu	ttt Phe 470	cac His	gta Val	aac Asn	ggc Gly	ggg Gly 475	tcg Ser	gtt Val	tca Ser	att Ile	tat Tyr 480	1440

gtt caa aga tag
Val Gln Arg

<210> 12
<211> 483
<212> PRT
<213> Künstliche Sequenz
<223> Beschreibung der künstlichen Sequenz:Fusion der
Alpha-Amylase-Gene von B. licheniformis und B.
amyloliquefaciens (AL256).

<400> 12
Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
1 5 10 15
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
20 25 30
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
35 40 45
Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
50 55 60
Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
65 70 75 80
Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
85 90 95
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
100 105 110
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
115 120 125
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
130 135 140
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145 150 155 160
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
165 170 175
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
180 185 190
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
195 200 205
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
210 215 220
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225 230 235 240
Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
245 250 255
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
260 265 270
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
275 280 285
His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Tyr Asp Met
290 295 300
Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala
305 310 315 320
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
325 330 335
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
340 345 350
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
355 360 365
Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
370 375 380
Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385 390 395 400

H04714.txt

Asp	Tyr	Phe	Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp
				405					410					415	
Ser	Ser	Val	Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro
			420					425					430		
Gly	Gly	Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr
		435					440					445			
Trp	His	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser
	450					455					460				
Glu	Gly	Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr
465					470					475					480
Val	Gln	Arg													

<210> 13
 <211> 1452
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen Sequenz: Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (ALA34-84).

<220>
 <221> CDS
 <222> (1)..(1452)

<400> 13	
gta aat ggc acg ctg atg cag tat ttt gaa tgg tat acg ccg aac gac	48
Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp	
1 5 10 15	
ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta tcg gat	96
Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp	
20 25 30	
atc ggt att act gcc gtc tgg att ccc ccg gca tat aag gga acg agc	144
Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser	
35 40 45	
caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta ggg gag	192
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu	
50 55 60	
ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa gga gag	240
Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu	
65 70 75 80	
ctg caa tct gcg atc ggc tca ctg cat tcc cgg aac gtc caa gta tac	288
Leu Gln Ser Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr	
85 90 95	
gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca gaa gat	336
Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp	
100 105 110	
gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act tcg	384
Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser	
115 120 125	
gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt	432
Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg	

130		135															
gga aac acg tac agt gat ttt aaa tgg cat tgg tat cat ttc gac gga	480																
Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly																	
145 150 155 160																	
gcg gac tgg gat gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt	528																
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg																	
165 170 175 180																	
ggg gaa gga aaa gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac	576																
Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn																	
185 190 195 200																	
tat gac tat tta atg tat gct gat gtt gac tac gac cac cct gat gtc	624																
Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val																	
195 200 205 210																	
gtg gca gag aca aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca	672																
Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser																	
210 215 220 225																	
tta gac ggc ttc cgt att gat gcc gcc aaa cat att aaa ttt tca ttt	720																
Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe																	
225 230 235 240																	
ctg cgt gat tgg gtt cag gcg gtc aga cag gcg acg gga aaa gaa atg	768																
Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met																	
245 250 255 260																	
ttt acg gtt gcg gag tat tgg cag aat aat gcc ggg aaa ctc gaa aac	816																
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn																	
260 265 270 275																	
tac ttg aat aaa aca agc ttt aat caa tcc gtg ttt gat gtt ccg ctt	864																
Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu																	
275 280 285 290																	
cat ttc aat tta cag gcg gct tcc tca caa gga ggc gga tat gat atg	912																
His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met																	
290 295 300 305																	
agg cgt ttg ctg gac ggt acc gtt gtg tcc agg cat ccg gaa aag gcg	960																
Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala																	
310 315 320 325																	
gtt aca ttt gtt gaa aat cat gac aca cag ccg gga cag tca ttg gaa	1008																
Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu																	
325 330 335 340																	
tcg aca gtc caa act tgg ttt aaa ccg ctt gca tac gcc ttt att ttg	1056																
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu																	
340 345 350 355																	
aca aga gaa tcc ggt tat cct cag gtg ttc tat ggg gat atg tac ggg	1104																
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly																	
355 360 365 370																	
aca aaa ggg aca tcg cca aag gaa att ccc tca ctg aaa gat aat ata	1152																
Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile																	
370 375 380 385																	
gag ccg att tta aaa gcg cgt aag gag tac gca tac ggg ccc cag cac	1200																
390 395 400 405																	

H04714.txt

Glu 385	Pro	Ile	Leu	Lys	Ala 390	Arg	Lys	Glu	Tyr	Ala 395	Tyr	Gly	Pro	Gln	His 400	
gat Asp	tat Tyr	att Ile	gac Asp	cac His 405	ccg Pro	gat Asp	gtg Val	atc Ile	gga Gly 410	tgg Trp	acg Thr	agg Arg	gaa Glu	ggt Gly 415	gac Asp	1248
agc Ser	tcc Ser	gcc Ala	gcc Ala 420	aaa Lys	tca Ser	ggt Gly	ttg Leu	gcc Ala 425	gct Ala	tta Leu	atc Ile	acg Thr	gac Asp 430	gga Gly	ccc Pro	1296
ggc Gly	gga Gly	tca Ser 435	aag Lys	cgg Arg	atg Met	tat Tyr	gcc Ala 440	ggc Gly	ctg Leu	aaa Lys	aat Asn	gcc Ala 445	ggc Gly	gag Glu	aca Thr	1344
tgg Trp	tat Tyr 450	gac Asp	ata Ile	acg Thr	ggc Gly	aac Asn 455	cgt Arg	tca Ser	gat Asp	act Thr	gta Val 460	aaa Lys	atc Ile	gga Gly	tct Ser	1392
gac Asp 465	ggc Gly	tgg Trp	gga Gly	gag Glu	ttt Phe 470	cat His	gta Val	aac Asn	gat Asp	ggg Gly 475	tcc Ser	gtc Val	tcc Ser	att Ile	tat Tyr 480	1440
ggt Val	cag Gln	aaa Lys	taa													1452

<210> 14
 <211> 483
 <212> PRT
 <213> Künstliche Sequenz
 <223> Beschreibung der künstlichen Sequenz: Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (ALA34-84).

<400> 14

Val 1	Asn	Gly	Thr	Leu 5	Met	Gln	Tyr	Phe	Glu 10	Trp	Tyr	Thr	Pro	Asn 15	Asp	
Gly	Gln	His	Trp 20	Lys	Arg	Leu	Gln	Asn 25	Asp	Ala	Glu	His	Leu 30	Ser	Asp	
Ile	Gly	Ile 35	Thr	Ala	Val	Trp	Ile 40	Pro	Pro	Ala	Tyr	Lys 45	Gly	Thr	Ser	
Gln	Ala	Asp	Val	Gly	Tyr	Gly 55	Ala	Tyr	Asp	Leu	Tyr 60	Asp	Leu	Gly	Glu	
Phe 65	His	Gln	Lys	Gly	Thr 70	Val	Arg	Thr	Lys 75	Tyr	Gly	Thr	Lys	Gly	Glu 80	
Leu	Gln	Ser	Ala	Ile 85	Gly	Ser	Leu	His 90	Ser	Arg	Asn 95	Val	Gln	Val	Tyr	
Gly	Asp	Val	Val 100	Leu	Asn	His	Lys	Ala 105	Gly	Ala	Asp	Ala	Thr 110	Glu	Asp	
Val	Thr	Ala 115	Val	Glu	Val	Asn	Pro 120	Ala	Asn	Arg	Asn 125	Gln	Glu	Thr	Ser	
Glu	Glu 130	Tyr	Gln	Ile	Lys	Ala 135	Trp	Thr	Asp	Phe	Arg 140	Phe	Pro	Gly	Arg	
Gly 145	Asn	Thr	Tyr	Ser	Asp 150	Phe	Lys	Trp	His 155	Trp	Tyr	His	Phe	Asp	Gly 160	
Ala	Asp	Trp	Asp	Glu 165	Ser	Arg	Lys	Ile	Ser 170	Arg	Ile	Phe	Lys	Phe 175	Arg	
Gly	Glu	Gly	Lys 180	Ala	Trp	Asp	Trp	Glu 185	Val	Ser	Ser	Glu	Asn 190	Gly	Asn	
Tyr	Asp	Tyr 195	Leu	Met	Tyr	Ala 200	Asp	Val	Asp	Tyr	Asp	His 205	Pro	Asp	Val	
Val	Ala	Glu	Thr	Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	Leu	Ser	

H04714.txt

210	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	Ser	Phe
225	Leu	Arg	Asp	Trp	Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	Glu	Met
	Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asn	Ala	Gly	Lys	Leu	Glu	Asn
	Tyr	Leu	Asn	Lys	Thr	Ser	Phe	Asn	Gln	Ser	Val	Phe	Asp	Val	Pro	Leu
	His	Phe	Asn	Leu	Gln	Ala	Ala	Ser	Ser	Gln	Gly	Gly	Gly	Tyr	Asp	Met
	Arg	Arg	Leu	Leu	Asp	Gly	Thr	Val	Val	Ser	Arg	His	Pro	Glu	Lys	Ala
305	Val	Thr	Phe	Val	Glu	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu
	Ser	Thr	Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu
	Thr	Arg	Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly
	Thr	Lys	Gly	Thr	Ser	Pro	Lys	Glu	Ile	Pro	Ser	Leu	Lys	Asp	Asn	Ile
385	Glu	Pro	Ile	Leu	Lys	Ala	Arg	Lys	Glu	Tyr	Ala	Tyr	Gly	Pro	Gln	His
	Asp	Tyr	Ile	Asp	His	Pro	Asp	Val	Ile	Gly	Trp	Thr	Arg	Glu	Gly	Asp
	Ser	Ser	Ala	Ala	Lys	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro
	Gly	Gly	Ser	Lys	Arg	Met	Tyr	Ala	Gly	Leu	Lys	Asn	Ala	Gly	Glu	Thr
	Trp	Tyr	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Asp	Thr	Val	Lys	Ile	Gly	Ser
465	Asp	Gly	Trp	Gly	Glu	Phe	His	Val	Asn	Asp	Gly	Ser	Val	Ser	Ile	Tyr
	Val	Gln	Lys													

<210> 15
 <211> 1458
 <212> DNA
 <213> Künstliche Sequenz

<220>
 <223> Beschreibung der künstlichen Sequenz:Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (LAL19-433).

<220>
 <221> CDS
 <222> (1)..(1458)

<400> 15																	
gca	aat	ctt	aat	ggg	acg	ctg	atg	cag	tat	ttt	gaa	tgg	tac	atg	ccc		48
Ala	Asn	Leu	Asn	Gly	Thr	Leu	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	Met	Pro		
1				5					10					15			
aat	gac	ggc	cag	cat	tgg	aaa	cga	ttg	cag	aat	gat	gcg	gaa	cat	tta		96
Asn	Asp	Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu		
			20					25					30				
tcg	gat	atc	gga	atc	act	gcc	gtc	tgg	att	cct	ccc	gca	tac	aaa	gga		144
Ser	Asp	Ile	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly		
		35					40					45					

H04714.txt

ttg	agc	caa	tcc	gat	aac	gga	tac	gga	cct	tat	gat	ttg	tat	gat	tta	192
Leu	Ser	Gln	Ser	Asp	Asn	Gly	Tyr	Gly	Pro	Tyr	Asp	Leu	Tyr	Asp	Leu	
	50					55					60					
gga	gaa	ttc	cag	caa	aaa	ggg	acg	gtc	aga	acg	aaa	tac	ggc	aca	aaa	240
Gly	Glu	Phe	Gln	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	
65					70					75					80	
tca	gag	ctt	caa	gat	gcg	atc	ggc	tca	ctg	cat	tcc	cgg	aac	gtc	caa	288
Ser	Glu	Leu	Gln	Asp	Ala	Ile	Gly	Ser	Leu	His	Ser	Arg	Asn	Val	Gln	
				85					90					95		
gta	tac	gga	gat	gtg	gtt	ttg	aat	cat	aag	gct	ggt	gct	gat	gca	aca	336
Val	Tyr	Gly	Asp	Val	Val	Leu	Asn	His	Lys	Ala	Gly	Ala	Asp	Ala	Thr	
			100					105					110			
gaa	gat	gta	act	gcc	gtc	gaa	gtc	aat	ccg	gcc	aat	aga	aat	cag	gaa	384
Glu	Asp	Val	Thr	Ala	Val	Glu	Val	Asn	Pro	Ala	Asn	Arg	Asn	Gln	Glu	
		115					120					125				
act	tcg	gag	gaa	tat	caa	atc	aaa	gcg	tgg	acg	gat	ttt	cgt	ttt	ccg	432
Thr	Ser	Glu	Glu	Tyr	Gln	Ile	Lys	Ala	Trp	Thr	Asp	Phe	Arg	Phe	Pro	
	130					135					140					
ggc	cgt	gga	aac	acg	tac	agt	gat	ttt	aaa	tgg	cat	tgg	tat	cat	ttc	480
Gly	Arg	Gly	Asn	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	
145					150					155					160	
gac	gga	gcg	gac	tgg	gat	gaa	tcc	cgg	aag	atc	agc	cgc	atc	ttt	aag	528
Asp	Gly	Ala	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Ile	Ser	Arg	Ile	Phe	Lys	
				165					170					175		
ttt	cgt	ggg	gaa	gga	aaa	gcg	tgg	gat	tgg	gaa	gta	tca	agt	gaa	aac	576
Phe	Arg	Gly	Glu	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Ser	Glu	Asn	
			180					185					190			
ggc	aac	tat	gac	tat	tta	atg	tat	gct	gat	gtt	gac	tac	gac	cac	cct	624
Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Val	Asp	Tyr	Asp	His	Pro	
		195					200					205				
gat	gtc	gtg	gca	gag	aca	aaa	aaa	tgg	ggt	atc	tgg	tat	gcg	aat	gaa	672
Asp	Val	Val	Ala	Glu	Thr	Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	
	210					215					220					
ctg	tca	tta	gac	ggc	ttc	cgt	att	gat	gcc	gcc	aaa	cat	att	aaa	ttt	720
Leu	Ser	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	
225					230					235					240	
tca	ttt	ctg	cgt	gat	tgg	gtt	cag	gcg	gtc	aga	cag	gcg	acg	gga	aaa	768
Ser	Phe	Leu	Arg	Asp	Trp	Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	
				245					250					255		
gaa	atg	ttt	acg	gtt	gcg	gag	tat	tgg	cag	aat	aat	gcc	ggg	aaa	ctc	816
Glu	Met	Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asn	Ala	Gly	Lys	Leu	
			260					265					270			
gaa	aac	tac	ttg	aat	aaa	aca	agc	ttt	aat	caa	tcc	gtg	ttt	gat	gtt	864
Glu	Asn	Tyr	Leu	Asn	Lys	Thr	Ser	Phe	Asn	Gln	Ser	Val	Phe	Asp	Val	
		275					280					285				
ccg	ctt	cat	ttc	aat	tta	cag	gcg	gct	tcc	tca	caa	gga	ggc	gga	tat	912
Pro	Leu	His	Phe	Asn	Leu	Gln	Ala	Ala	Ser	Ser	Gln	Gly	Gly	Gly	Tyr	

H04714.txt
300

290	295																
gat atg agg cgt ttg ctg gac ggt acc gtt gtg tcc agg cat ccg gaa Asp Met Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu 305 310 315 320																	960
aag gcg gtt aca ttt gtt gaa aat cat gac aca cag ccg gga cag tca Lys Ala Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser 325 330 335																	1008
ttg gaa tcg aca gtc caa act tgg ttt aaa ccg ctt gca tac gcc ttt Leu Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe 340 345 350																	1056
att ttg aca aga gaa tcc ggt tat cct cag gtg ttc tat ggg gat atg Ile Leu Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met 355 360 365																	1104
tac ggg aca aaa ggg aca tcg cca aag gaa att ccc tca ctg aaa gat Tyr Gly Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp 370 375 380																	1152
aat ata gag ccg att tta aaa gcg cgt aag gag tac gca tac ggg ccc Asn Ile Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro 385 390 400																	1200
cag cac gat tat att gac cac ccg gat gtg atc gga tgg acg agg gaa Gln His Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu 405 410 415																	1248
ggt gac agc tcc gcc gcc aaa tca ggt ttg gcc gct tta atc acg gac Gly Asp Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp 420 425 430																	1296
gga ccc ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly 435 440 445																	1344
gag aca tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile 450 455 460																	1392
aat tcg gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca Asn Ser Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser 465 470 475 480																	1440
att tat gtt caa aga tag Ile Tyr Val Gln Arg 485																	1458

<210> 16
 <211> 485
 <212> PRT
 <213> Künstliche Sequenz
 <223> Beschreibung der künstlichen Sequenz:Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (LAL19-433).

<400> 16
 Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
 1 5 10 15
 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu
 Page 26

H04714.txt

```

      20      25      30
Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
      35      40      45
Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu
      50      55      60
Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
      65      70      75      80
Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln
      85      90      95
Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr
      100      105      110
Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu
      115      120      125
Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro
      130      135      140
Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
      145      150      155      160
Asp Gly Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys
      165      170      175
Phe Arg Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn
      180      185      190
Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro
      195      200      205
Asp Val Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu
      210      215      220
Leu Ser Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe
      225      230      235      240
Ser Phe Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys
      245      250      255
Glu Met Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu
      260      265      270
Glu Asn Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val
      275      280      285
Pro Leu His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr
      290      295      300
Asp Met Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu
      305      310      315
Lys Ala Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser
      320      325      330
Leu Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe
      335      340      345
Ile Leu Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met
      350      355      360
Tyr Gly Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp
      365      370      375
Asn Ile Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro
      380      385      390
Gln His Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu
      395      400      405
Gly Asp Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp
      410      415      420
Gly Pro Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly
      425      430      435
Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile
      440      445      450
Asn Ser Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser
      455      460      465
Ile Tyr Val Gln Arg
      470      475      480
      485

```

<211> 1452

<212> DNA

<213> Künstliche Sequenz

<220>

<223> Beschreibung der künstlichen Sequenz: Fusion der
Alpha-Amylase-Gene von B. licheniformis und B.
amyloliquefaciens (LAL19-153).

<220>

<221> CDS

<222> (1)..(1452)

<400> 17

gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc	48
Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro	
1 5 10 15	
aat gac ggc cag cat tgg aaa cga ttg cag aat gat gcg gaa cat tta	96
Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu	
20 25 30	
tcg gat atc gga atc act gcc gtc tgg att cct ccc gca tac aaa gga	144
Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly	
35 40 45	
ttg agc caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta	192
Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu	
50 55 60	
gga gaa ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa	240
Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys	
65 70 75 80	
tca gag ctt caa gat gcg atc ggc tca ctg cat tcc cgg aac gtc caa	288
Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln	
85 90 95	
gta tac gga gat gtg gtt ttg aat cat aag gct ggt gct gat gca aca	336
Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr	
100 105 110	
gaa gat gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa	384
Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu	
115 120 125	
act tcg gag gaa tat caa atc aaa gcg tgg acg gat ttt cgt ttt ccg	432
Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro	
130 135 140	
ggc cgt gga aac acg tac agt gat ttt aaa tgg cat tgg tac cat ttt	480
Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe	
145 150 155 160	
gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag	528
Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys	
165 170 175	
ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac	576
Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn	
180 185 190	
tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc	624

H04714.txt

Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Ile	Asp	Tyr	Asp	His	Pro	Asp	Val		
		195					200					205					
gca	gca	gaa	att	aag	aga	tgg	ggc	act	tgg	tat	gcc	aat	gaa	ctg	caa	672	
Ala	Ala	Glu	Ile	Lys	Arg	Trp	Gly	Thr	Trp	Tyr	Ala	Asn	Glu	Leu	Gln		
	210					215					220						
ttg	gac	ggt	ttc	cgt	ctt	gat	gct	gtc	aaa	cac	att	aaa	ttt	tct	ttt	720	
Leu	Asp	Gly	Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe		
225					230					235					240		
ttg	cgg	gat	tgg	gtt	aat	cat	gtc	agg	gaa	aaa	acg	ggg	aag	gaa	atg	768	
Leu	Arg	Asp	Trp	Val	Asn	His	Val	Arg	Glu	Lys	Thr	Gly	Lys	Glu	Met		
				245					250					255			
ttt	acg	gta	gct	gaa	tat	tgg	cag	aat	gac	ttg	ggc	gcg	ctg	gaa	aac	816	
Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn		
			260					265					270				
tat	ttg	aac	aaa	aca	aat	ttt	aat	cat	tca	gtg	ttt	gac	gtg	ccg	ctt	864	
Tyr	Leu	Asn	Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu		
		275					280					285					
cat	tat	cag	ttc	cat	gct	gca	tcg	aca	cag	gga	ggc	ggc	tat	gat	atg	912	
His	Tyr	Gln	Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met		
	290					295					300						
agg	aaa	ttg	ctg	aac	agt	acg	gtc	gtt	tcc	aag	cat	ccg	ttg	aaa	gcg	960	
Arg	Lys	Leu	Leu	Asn	Ser	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ala		
305					310					315					320		
gtt	aca	ttt	gtc	gat	aac	cat	gat	aca	cag	ccg	ggg	caa	tcg	ctt	gag	1008	
Val	Thr	Phe	Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu		
				325					330					335			
tcg	act	gtc	caa	aca	tgg	ttt	aag	ccg	ctt	gct	tac	gct	ttt	att	ctc	1056	
Ser	Thr	Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu		
			340					345					350				
aca	agg	gaa	tct	gga	tac	cct	cag	gtt	ttc	tac	ggg	gat	atg	tac	ggg	1104	
Thr	Arg	Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly		
		355					360					365					
acg	aaa	gga	gac	tcc	cag	cgc	gaa	att	cct	gcc	ttg	aaa	cac	aaa	att	1152	
Thr	Lys	Gly	Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile		
	370					375					380						
gaa	ccg	atc	tta	aaa	gcg	aga	aaa	cag	tat	gcg	tac	gga	gca	cag	cat	1200	
Glu	Pro	Ile	Leu	Lys	Ala	Arg	Lys	Gln	Tyr	Ala	Tyr	Gly	Ala	Gln	His		
385					390					395					400		
gat	tat	ttc	gac	cac	cat	gac	att	gtc	ggc	tgg	aca	agg	gaa	ggc	gac	1248	
Asp	Tyr	Phe	Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp		
				405					410					415			
agc	tcg	gtt	gca	aat	tca	ggt	ttg	gcg	gca	tta	ata	aca	gac	gga	ccc	1296	
Ser	Ser	Val	Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro		
			420					425					430				
ggt	ggg	gca	aag	cga	atg	tat	gtc	ggc	cgg	caa	aac	gcc	ggt	gag	aca	1344	
Gly	Gly	Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr		
		435					440					445					

H04714.txt

tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg 1392
 Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
 450 455 460

gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat 1440
 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480

gtt caa aga tag 1452
 Val Gln Arg

<210> 18

<211> 483

<212> PRT

<213> Künstliche Sequenz

<223> Beschreibung der künstlichen Sequenz:Fusion der
 Alpha-Amylase-Gene von B. licheniformis und B.
 amyloliquefaciens (LAL19-153).

<400> 18

Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
 1 5 10 15
 Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu
 20 25 30
 Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
 35 40 45
 Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu
 50 55 60
 Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
 65 70 75 80
 Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln
 85 90 95
 Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr
 100 105 110
 Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu
 115 120 125
 Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro
 130 135 140
 Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
 145 150 155 160
 Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
 165 170 175
 Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
 180 185 190
 Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
 195 200 205
 Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
 210 215 220
 Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
 225 230 235 240
 Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
 245 250 255
 Phe Thr Val Ala Glu Tyr Trp Gln Asn His Ser Val Phe Asp Val Pro Leu
 260 265 270
 Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
 275 280 285
 His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
 290 295 300
 Arg Lys Leu Leu Asn Ser Thr Val Val Ser Lys His Pro Leu Lys Ala
 305 310 315 320
 Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335

H04714.txt

Ser	Thr	Val	Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu
			340					345					350		
Thr	Arg	Glu	Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly
		355					360					365			
Thr	Lys	Gly	Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile
	370					375					380				
Glu	Pro	Ile	Leu	Lys	Ala	Arg	Lys	Gln	Tyr	Ala	Tyr	Gly	Ala	Gln	His
385					390					395					400
Asp	Tyr	Phe	Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp
				405					410					415	
Ser	Ser	Val	Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro
			420					425					430		
Gly	Gly	Ala	Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr
		435					440					445			
Trp	His	Asp	Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser
	450					455					460				
Glu	Gly	Trp	Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr
465					470					475					480
Val	Gln	Arg													